FIG. 1A

```
  1   TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGGGGAGCC    60


 61   TCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGATAGGGCGAGGCT   120


121   GTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGG   180
  1                                      M   A   S   S   I   L   K   W   V   V    10


181   TCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGG   240
 11    S   H   Q   S   C   S   R   S   S   R   S   K   P   R   D   Q   R   E   E   A    30


241   CCGGGAGCAGCGACCTGAGCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGG   300
 31    G   S   S   D   L   S   S   R   Q   D   A   E   N   A   E   A   K   L   R   G    50


301   GCCTCCCGGGGCAGCTTGTGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGC   360
 51    L   P   G   Q   L   V   D   I   A   C   K   V   C   Q   A   Y   L   G   Q   L    70


361   TGGAGCATGAGGACATCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGT   420
 71    E   H   E   D   I   D   T   S   A   D   A   V   E   D   L   T   E   A   E   W    90


421   GGGAGGACCTGACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATT   480
 91    E   D   L   T   Q   Q   Y   Y   S   L   V   H   G   D   A   F   I   S   N   S   110


481   CAAGAAATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC   540
111    R   N   Y   F   S   Q   C   Q   A   L   L   N   R   I   T   S   V   N   P   Q   130


541   AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGG   600
131    T   D   I   D   G   L   R   N   I   W   I   I   K   P   A   A   K   S   R   G   150


601   GCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACC   660
151    R   D   I   V   C   M   D   R   V   E   E   I   L   E   L   A   A   A   D   H   170


661   ACCCTCTTTCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCA   720
171    P   L   S   R   D   N   K   W   V   V   Q   K   Y   I   E   T   P   L   L   I   190


721   TCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGA   780
191    C   D   T   K   F   D   I   R   Q   W   F   L   V   T   D   W   N   P   L   T   210


781   CCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACA   840
211    I   W   F   Y   K   E   S   Y   L   R   F   S   T   Q   R   F   S   L   D   K   230
```

FIG. 1B

```
 841  AGCTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATG   900
 231    L  D  S  A  I  H  L  C  N  N  A  V  Q  K  Y  L  K  N  D  V   250

 901  TGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGT   960
 251    G  R  S  P  L  L  P  A  H  N  M  W  T  S  T  R  F  Q  E  Y   270

 961  ACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGA  1020
 271    L  Q  R  Q  G  R  G  A  V  W  G  S  V  I  Y  P  S  M  K  K   290

1021  AGGCCATCGCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCT  1080
 291    A  I  A  H  A  M  K  V  A  Q  D  H  V  E  P  R  K  N  S  F   310

1081  TTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGA  1140
 311    E  L  Y  G  A  D  F  V  L  G  R  D  F  R  P  W  L  I  E  I   330

1141  TCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGG  1200
 331    N  S  S  P  T  M  H  P  S  T  P  V  T  A  Q  L  C  A  Q  V   350

1201  TGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGC  1260
 351    Q  E  D  T  I  K  V  A  V  D  R  S  C  D  I  G  N  F  E  L   370

1261  TCCTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGG  1320
 371    L  W  R  Q  P  V  V  E  P  P  P  F  S  G  S  D  L  C  V  A   390

1321  CGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT  1380
 391    G  V  S  V  R  R  A  R  R  Q  V  L  P  V  C  N  L  K  A  S   410

1381  CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACC  1440
 411    A  S  L  L  D  A  Q  P  L  K  A  R  G  P  S  A  M  P  D  P   430

1441  CTGCCCAGGGACCCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGG  1500
 431    A  Q  G  P  P  S  P  A  L  Q  R  D  L  G  L  K  E  E  K  G   450

1501  GGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCAC  1560
 451    L  P  L  A  L  L  A  P  L  R  G  A  A  E  S  G  G  A  A  Q   470

1561  AGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACG  1620
 471    P  T  R  T  K  A  A  G  K  V  E  L  P  A  C  P  C  R  H  V   490

1621  TGGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATC  1680
 491    D  S  Q  A  P  N  T  G  V  P  V  A  Q  P  A  K  S  W  D  P   510
```

FIG. 1C

```
1681  CAAACCAGCTAAATGCGCACCCGCTGGAGCCTGTGCTGCGGGGCCTGAAGACAGCAGAGG   1740
511     N   Q   L   N   A   H   P   L   E   P   V   L   R   G   L   K   T   A   E   G   530


1741  GCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCA   1800
531     A   L   R   P   P   P   G   G   K   G   S   541


1801  GGAGTACAGGTTGCAGCCACTCTCCCAAGGGCGAATTC   1838
```

FIG. 2

```
  1 ATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGAC   60
  1  I   D   G   L   R   N   I   W   I   I   K   P   A   A   K   S   R   G   R   D    20


 61 ATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTT  120
 21  I   V   C   M   D   R   V   E   E   I   L   E   L   A   A   A   D   H   P   L    40


121 TCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGAC  180
 41  S   R   D   N   K   W   V   V   Q   K   Y   I   E   T   P   L   L   I   C   D    60


181 ACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGG  240
 61  T   K   F   D   I   R   Q   W   F   L   V   T   D   W   N   P   L   T   I   W    80


241 TTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGAC  300
 81  F   Y   K   E   S   Y   L   R   F   S   T   Q   R   F   S   L   D   K   L   D   100


301 AGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGC  360
101  S   A   I   H   L   C   N   N   A   V   Q   K   Y   L   K   N   D   V   G   R   120


361 AGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAG  420
121  S   P   L   L   P   A   H   N   M   W   T   S   T   R   F   Q   E   Y   L   Q   140


421 CGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATC  480
141  R   Q   G   R   G   A   V   W   G   S   V   I   Y   P   S   M   K   K   A   I   160


481 GCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTC  540
161  A   H   A   M   K   V   A   Q   D   H   V   E   P   R   K   N   S   F   E   L   180


541 TACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCC  600
181  Y   G   A   D   F   V   L   G   R   D   F   R   P   W   L   I   E   I   N   S   200


601 AGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG  660
201  S   P   T   M   H   P   S   T   P   V   T   A   Q   L   C   A   Q   V   Q   E   220


661 GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGG  720
221  D   T   I   K   V   A   V   D   R   S   C   D   I   G   N   F   E   L   L   W   240


721 AGGCAG   726
241  R   Q    242
```

FIG. 3A

```
           1                                                    50
BGS-42    (1)   --------MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAE
TTL_PIG   (1)   MYTFVVRDENSSVYAEVSRLLLATGHWKRLRRDNPRFNLMLGERNRLPFG
TTLL_Hu   (1)   --------MAGKVKWVTDIEKSVLINNFEKRGWVQVTENEDWNFYWMSV
TTLH_Hu   (1)   --------------------------------------------------
HOTTL     (1)   --------------------------------------------------

           51                                                   100
BGS-42    (43)  NAEAKLRGLPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWED
TTL_PIG   (51)  RLGHEPGLMQLVNYYRGADKLCRKASLVKLIKTSPELAESCTWFPESYVI
TTLL_Hu   (42)  QTIRNVFSVEAGYRLSDDQIVNHFP--NHYELTRKDLMVKN--IKRYRKE
TTLH_Hu   (1)   -----------------------------MDIDKDLEAPLYLTPEGWSL
HOTTL     (1)   --------------------------------------------------

           101                                                  150
BGS-42    (93)  LTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGLRNIWII
TTL_PIG   (101) YPTNLKTPVAPAQNGIHPPIHSSRTDEREFFLTSYNKKKE-DGEGNVWIA
TTLL_Hu   (88)  LEKEGSPLAEKDENGKYLYLDFVPVTYMLPADYNLFVEEFRKSPSSTWIM
TTLH_Hu   (21)  FLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIV
HOTTL     (1)   ------------------------------------MEGDRNFWIV

           151                                                  200
BGS-42    (143) KPAAKSRGRDIVCMDRVEEILELAAADHPLSRDN-----KWVVQKYIETP
TTL_PIG   (150) KSSAGAKGEGILISSEATELLDFIDN------QGQ----VHVIQKYLERP
TTLL_Hu   (138) KPCGKAQGKGIFLTNKLSQIKKWSRDSKTSSFVSQSNKEAYVISLYINNP
TTLH_Hu   (71)  KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP
HOTTL     (11)  KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP

           201                                                  250
BGS-42    (188) LLICD--TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSA-
TTL_PIG   (190) LILEPGHRKFDIRSWVLVD--HQYNIYLYREGVLRTASEPYHTDNFQDKT
TTLL_Hu   (188) LLIGG--RKFDLRLYVLVSTYRPLRCYMYKLGFCRFCTVKYTPSTSELDN
TTLH_Hu   (116) LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-
HOTTL     (56)  LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-

           251                                                  300
BGS-42    (235) --IHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGS
TTL_PIG   (238) --CHLTNHCIQKEYSKNYGKYE--E-GNEMFFEEFNQYITSAL-NITLES
TTLL_Hu   (236) MFVHLTNVAIQKHGEDYNHIH---G--GKWTVSNLRLYLESTR-GKEVTS
TTLH_Hu   (163) --VHLCNNSIQKHLENSCHRHPLLPPDNMWSSQRFQAHLQEMGAPNAWST
HOTTL     (103) --VHLCNNSIQKHLENSCHRHPLLPPDNMWSSQRFQAHLQEMGAPNAWST

           301                                                  350
BGS-42    (283) VIYPSMKKAIAHAMKVAQDHVEPRKN---SFELYGADFVLGRDFRPWLIE
TTL_PIG   (282) SILLQIKHIIRSCLLSVEPAISTRHLPYQSFQLFGFDFMVDEDLKVWLIE
TTLL_Hu   (280) KLFDEIHWIIVQSLKAVAPVMNNDKH---CFECYGYDIIIDDKLKPWLIE
TTLH_Hu   (211) IIVPGMKDAVIHALQTSQDTVQCRKA---SFELYGADFVFGEDFQPWLIE
HOTTL     (151) IIVPGMKDAVIHALQTSQDTVQCRKA---SFELYGADFVFGEDFQPWLIE
```

FIG. 3B

```
        351                                                      400
BGS-42  (330)  INSSPTMHPSTPVTAQLCAQVQEDTIKVAVD-------------RSCDIG
TTL_PIG (332)  VNG------APACAQKLYAELCQGIVDIAIAS------------------
TTLL_Hu (327)  VNASPSLTSSTANDRILKYNLINDTLNIAVPNGEIPDCKWNKSPPKEVLG
TTLH_Hu (258)  INASPTMAPSTAVTARLCAGVQADTLRVVIDR---------MLDRNCDTG
HOTTL   (198)  INASPTMAPSTAVTARLCAGVQADTLRVVIDR---------MLDRNCDTG

        401                                                      450
BGS-42  (367)  NFEILWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDA
TTL_PIG (358)  VFPPPDAEQQQQ----QPPPAAFIKL------------------------
TTLL_Hu (377)  NYEIIYDEEIAQGDGADRELRSRQGQSLGPRAGR-----SRDSGRAVLTT
TTLH_Hu (299)  AFELIYKQPVTTSPASTPRPSCLLPMYSDTRAR-------SSDDSTASW
HOTTL   (239)  AFELIYKQPVTTSPASTPRPSCLLPMYSDTRAR-------SSDDSTASW

        451                                                      500
BGS-42  (417)  QPLKARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESG
TTL_PIG (380)  -------------------------------------------------
TTLL_Hu (422)  WK-----------------------------------------------
TTLH_Hu (341)  WALRPCRPQARP-------------------------------------
HOTTL   (281)  WALRPCRPQARP-------------------------------------

        501                                                      550
BGS-42  (467)  GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAH
TTL_PIG (380)  -------------------------------------------------
TTLL_Hu (424)  -------------------------------------------------
TTLH_Hu (353)  -------------------------------------------------
HOTTL   (293)  -------------------------------------------------

        551                 575
BGS-42  (517)  PLEPVLRGLKTAEGALRPPPGGKGS
TTL_PIG (380)  -------------------------
TTLL_Hu (424)  -------------------------
TTLH_Hu (353)  -------------------------
HOTTL   (293)  -------------------------
```

FIG. 4

Model	Description	Score	E-value	N
TTL	Tubulin-tyrosine ligase family	293.0	3.7e-84	1

```
Q    73 EDIDTS----ADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSR-------NYFSQCQALL
        ++ID +    +++ ++ + W   ++ ++  ++  + +         ++  +++++
T     1 MRIDMHYRMMHQMINHFPGSYWITRKDRLWMNIKRMMCDFHWKHDHFDWMPRTFILPTDY

Q   122 NRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAA-----ADHPLSRDN
        +++ +   ++ + +G++N+WI+KP++++RGR+I++M+  ++I+ ++      +P++ ++
T    61 QEFVDYWQKHEWWGQDNHWIVKPWNSCRGRGIWIMNDWKQIPRWVNDFMDNPFVPQHQRR

Q   177 KWVVQKYIETPLLICD-----TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFS--LD
        +WVVQKYIE PLLI        +KFDIR+++LVT++NPL+I++Y+E+++RF+++ ++   +
T   121 PWVVQKYIERPLLIDGMDVGHHKFDIRCYVLVTSFNPLRIYVYREGWCRFCSVKYHPMDN

Q   230 KLDSAIHLCNNAVQKYLKN--DVGRSPLLPAHNMWTSTRFQEYLQR--QGRGAVWGSVIY
        +  +HL+N+++QK+ +N    +R ++++ ++MWT  +F++Y+++   +  ++W +++
T   181 FDNYCMHLTNYCIQKHYSNYSRCNRDYNECHGHMWTLQNFWNYYENMGIDWDNIWSQICD

Q   286 PSMKKAIAHA-MKVAQDHVEPRKNSFELYGADFVL----GRDFRPWLIEINSSPTMHPST
        + +K+++A++ +++++++++PR+N+FELYG+DF +     +++ PWL+E+N+SP+MH+++
T   241 IIIKTIVAAWCVEACRMNMQPRYNCFELYGFDFMIQWDDDENLKPWLLEVNWSPDMHCTC

Q   341 PVTAQLCAQVQEDTIK-----VAVDRSCDI
        P+++ LC+Q+++D+++      V +D++ D+
T   301 PYDMHLCHQLIRDVLNCAGCHVPPDCMKDC
```

FIG. 5A

BGS-42 – Clone A

TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGG
GGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGAT
AGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGC
ATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAG
CCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCAAGA
TGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACAT
CGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCGA
CACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGAC
CCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATT
ACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGAC
GGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCG
GGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTC
ATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACC
CCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTT
CTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAACACCGTCCAGAA
GTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTG
GACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTG
GGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCATGAAGGT
GGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGA
CTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCC
ACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG
GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTC
CTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCATTCAGCGGGTCCGACCTCTGCG
TGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACC
TCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCT
CGGCCATGCCAGACCCTGCCCAGGGACCCCATCACCAGCTCTCCAGCGGGACTT
GGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGG
GGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAA
GGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACAC
CGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGA
GCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCG
TCCGCCGCCCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAG
TACAGGTTGCAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGT
CTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAG
CTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTCAATTTGATTTTTACTTATTCAACC
TGGAATTTGAATGTCAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:9)

FIG. 5B

BGS-42 – Clone B
GTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAGACTTCCGGCGCACCATGGCATC
CAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAG
CAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGC
AAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGG
ACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACA
TCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACC
TGACCCAGCAGTACTACTCCCTCGTTCATGCCAGGCTCTGCTGAATAGAATCACG
TCTGTGAACCCTCAGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGC
CCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGA
TCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGGTGGT
CCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCGACATCAG
ACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGGAG
AGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCA
TCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCA
GCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCT
GCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAA
GAAGGCCATCGCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAA
GAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCC
TGGCTGATCGAGATCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGG
CCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCA
GCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCGCCCCCA
TTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGG
CAGGTGCTGCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGC
CGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCAT
CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGG
CCTTGCTGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCA
CCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGT
GGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTG
GGATCCAAACCAGCTAAATGAGCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAA
GACAGCAGAGGGCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTCATGACAGCG
TCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCCACTCTCCCGCCGAACATTGA
ATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTC
AGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTC
AATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAAAAAAA
AAAAAAAA (SEQ ID NO:10)

FIG. 5C

BGS-42 – Clone C

CCCAGGACTCCTGGTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCCACCC
CCAGCACCCCTGTGCCCTTTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAA
GCTCCCTCCTCAGGGCACAGAGGCCAAAGATGGGGCTGACTGGGGGCTGCCACC
GGGCTTTGGGTGCTGAGGGGGCTGTGGGACCCCAGGGGAAGAGGTGCCGCTCCC
CCCAGCACCGGGCACTCCCCCGCCTCCCCGGCCTCCAGCCCTGCACAAAGCAGC
TTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTGCCCAGGACGCAGGG
TGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCTGGCACAGA
GGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAGGT
GCAGGACAAGGTTCCCTTCCGCACCTAATACCCCAGGGTCAGGCCAGCGCCAGC
GCTGCTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGC
GTGCGCTGTGTTTCTGGGGGCCAGCCACTTTTTTCCTTAACGGGGTGACAAACC
AGACATCGGGGTGCGGGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCT
CGCGTGTGGTGGGCAGTGCTGGGCATGTGGCTGCGTTCCGGGCCCTGCAGCCGCT
CCTCCCTCTCCTGGGGTCTGAGGTGTGGGACACCCTGTGGCCCGTTTGGGGGCCT
GGAGGGAGCCCCAGTGCCCACCGCCCTCGGTGCCCTCAGCTGCAGCCTCCCCATT
CCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGGATGCGTCTGAGCCTGGCCTG
CACATCCATGCTCCCACCGGCTGGAGGGGGTGTTCTGGGGCCCTGGGGGACCGT
ATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTGCCCCATAG
CCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAGCT
GAGCTGAGCTGCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTG
CGTGAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTC
CCACGCTGCTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAG
TGAGGAGACGGCAGAGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGAT
CCCCCTGGTGCTGAGACAGACTGATGGGGCAGGGTCTGAGGATAGAGGACCGGG
GAGAGGCCTCCCATGGTCATGGTCATGGCAGTACAGAGGCCAGGGGCCCCGGGA
GGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTCTGTGCTAGGCTTGTGGACAGCG
CGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGAGGCCGAGGGGTGCAGC
TGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGCAGACTGGGG
GTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGT
TGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACA
GATAGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCC
AGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGC
AAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCA
AGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGA
CATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACAT
CGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCT
GACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGA
AATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC
AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGT
CCCGGGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCT
GCTCATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGG
AACCCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGC
GCTTCTCCCTGGACAAG

FIG. 5C (CONT.)

CTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAA
GAATGATGTGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCAC
CAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGT
CATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCATGAAGGTGGCCCAGGA
CCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTT
GGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCAC
CCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATC
AAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGG
CAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGGCGGGCG
TCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT
CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGC
CAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGA
AGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGGGGCAGCCG
AGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGC
TCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACACCGGTGTCCC
CGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGCACCCGCT
GGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGCC
CGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTG
CAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGT
GGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGT
TCTATCTGCCAGCTTTTGAGTGTTCAATTTGATTTTTACTTATTCAACCTGGAATTT
GAATGTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:11)

FIG. 6A

```
   1  GTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCCACCCCCAGCACCCCTGTGCCCT    60

  61  TTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAAGCTCCCTCCTCAGGGCACAGAGG   120

 121  CCAAAGATGGGGCTGACTGGGGGCTGCCACCGGGCTTTGGGTGCTGAGGGGGCTGTGGGA   180

 181  CCCCAGGGGAAGAGGTGCCGCTCCCCCCAGCACCGGGCACTCCCCCGCCTCCCCCGGCCT   240

 241  CCAGCCCTGCACAAAGCAGCTTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTG   300

 301  CCCAGGACGCAGGGTGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGCTTCCCT   360

 361  GGCACAGAGGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAG   420

 421  GTGCAGGACAAGGTTCCCTTCCGCACCTAATACCCCAGGGTCAGGCCAGCGCCAGCGCTG   480

 481  CTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGCGTGCGCTGTG   540

 541  TTTTCTGGGGGCCAGCCACTTTTTTCCTTAACGGGGTGACAAACCAGACATCGGGGTGCG   600

 601  GGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCTCGCGTGTGGTGGGCAGTGCT   660

 661  GGGCATGTGGCTGCGTTCCGGGCCCTGCAGCCGCTCCTCCCTCCTGGGGTCTGAGGTG   720

 721  TGGGACACCCTGTGGCCCGTTTGGGGGCCTGGAGGGAGCCCCAGTGCCCACCGCCCTCGG   780

 781  TGCCCTCAGCTGCAGCCTCCCCATTCCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGG   840

 841  ATGCGTCTGAGCCTGGCCTGCACATCCATGCTCCCACCGGCTGGAGGGGGTGTTCTGGGG   900

 901  CCCTGGGGGACCGTATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTG   960

 961  CCCCATAGCCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAG  1020

1021  CTGAGCTGAGCTGCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTGCGT  1080

1081  GAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTCCCACGCTG  1140
```

FIG. 6B

```
1141  CTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAGTGAGGAGACGGCAG   1200


1201  AGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGATCCCCCTGGTGCTGAGACAGA   1260


1261  CTGATGGGGCAGGGTCTGAGGATAGAGGACCGGGGAGAGGCCTCCCATGGTCATGGTCAT   1320


1321  GGCAGTACAGAGGCCAGGGGCCCCGGGAGGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTC   1380


1381  TGTGCTAGGCTTGTGGACAGCGCGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGA   1440


1441  GGCCGAGGGGTGCAGCTGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGC   1500


1501  AGACTGGGGGTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCG   1560


1561  GGTTGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGA   1620


1621  TAGGGCGAGGCTGTGCTGTCCTTTCAGAGTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAG   1680


1681  ACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCA   1740
   1            M   A   S   S   I   L   K   W   V   V   S   H   Q   S   C   S    16


1741  GCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGA   1800
  17    R   S   S   R   S   K   P   R   D   Q   R   E   E   A   G   S   S   D   L   S    36


1801  GCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTG   1860
  37    S   R   Q   D   A   E   N   A   E   A   K   L   R   G   L   P   G   Q   L   V    56


1861  TGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCG   1920
  57    D   I   A   C   K   V   C   Q   A   Y   L   G   Q   L   E   H   E   D   I   D    76


1921  ACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGACCCAGC   1980
  77    T   S   A   D   A   V   E   D   L   T   E   A   E   W   E   D   L   T   Q   Q    96


1981  AGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGC   2040
  97    Y   Y   S   L   V   H   G   D   A   F   I   S   N   S   R   N   Y   F   S   Q    116


2041  AGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGACGGACATTGACGGGC   2100
 117    C   Q   A   L   L   N   R   I   T   S   V   N   P   Q   T   D   I   D   G   L    136
```

FIG. 6C

```
2101 TCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCA 2160
137    R   N   I   W   I   I   K   P   A   A   K   S   R   G   R   D   I   V   C   M   156


2161 TGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACA 2220
157    D   R   V   E   E   I   L   E   L   A   A   A   D   H   P   L   S   R   D   N   176


2221 ACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCG 2280
177    K   W   V   V   Q   K   Y   I   E   T   P   L   L   I   C   D   T   K   F   D   196


2281 ACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGG 2340
197    I   R   Q   W   F   L   V   T   D   W   N   P   L   T   I   W   F   Y   K   E   216


2341 AGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCC 2400
217    S   Y   L   R   F   S   T   Q   R   F   S   L   D   K   L   D   S   A   I   H   236


2401 ACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGC 2460
237    L   C   N   N   A   V   Q   K   Y   L   K   N   D   V   G   R   S   P   L   L   256


2461 TGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCC 2520
257    P   A   H   N   M   W   T   S   T   R   F   Q   E   Y   L   Q   R   Q   G   R   276


2521 GTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCA 2580
277    G   A   V   W   G   S   V   I   Y   P   S   M   K   K   A   I   A   H   A   M   296


2581 TGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTG 2640
297    K   V   A   Q   D   H   V   E   P   R   K   N   S   F   E   L   Y   G   A   D   316


2641 ACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCA 2700
317    F   V   L   G   R   D   F   R   P   W   L   I   E   I   N   S   S   P   T   M   336


2701 TGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCA 2760
337    H   P   S   T   P   V   T   A   Q   L   C   A   Q   V   Q   E   D   T   I   K   356


2761 AGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGGCAGCCGG 2820
357    V   A   V   D   R   S   C   D   I   G   N   F   E   L   L   W   R   Q   P   V   376


2821 TGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGA 2880
377    V   E   P   P   P   F   S   G   S   D   L   C   V   A   G   V   S   V   R   R   396


2881 GAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACG 2940
397    A   R   R   Q   V   L   P   V   C   N   L   K   A   S   A   S   L   L   D   A   416
```

FIG. 6D

```
2941  CGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCAT  3000
 417   Q   P   L   K   A   R   G   P   S   A   M   P   D   P   A   Q   G   P   P   S   436


3001  CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGC  3060
 437   P   A   L   Q   R   D   L   G   L   K   E   E   K   G   L   P   L   A   L   L   456


3061  TGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAG  3120
 457   A   P   L   R   G   A   A   E   S   G   G   A   A   Q   P   T   R   T   K   A   476


3121  CTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAA  3180
 477   A   G   K   V   E   L   P   A   C   P   C   R   H   V   D   S   Q   A   P   N   496


3181  ACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGC  3240
 497   T   G   V   P   V   A   Q   P   A   K   S   W   D   P   N   Q   L   N   E   H   516


3241  ACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGC  3300
 517   P   L   E   P   V   L   R   S   L   K   T   A   E   G   A   L   R   P   P   P   536


3301  CCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCC  3360
 537   G   G   K   G   S                                               541


3361  ACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGG  3420


3421  AAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTT  3480


3481  TTGAGTGTTCAATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAA  3540


3541  AAAAAAAAAAAAA  3554
```

```
-2057   tgcctgcagcagagcccggctgggatcctcacgctgcacgccatttgtcctctgatggtt   -1998

-1997   gcctcactccatcccatcctggctggtgtgaaccttgaatgctgggcatcaataaagact   -1938

-1937   tttttcttgccagtctaggttggtaaaaaatgagatgccgtacctcctctggaccatcaa   -1878

-1877   gagggacatcattgactatcacagcctgacctacgaccagatgctgaaccactacgcaaa   -1818

-1817   gacagcctccttcaccaccaaggtgagccggccgcgcttgagcgtggcgggagccggcaa   -1758

-1757   gggtggtggggaggagcttctgcagccattagggaccctcggtggctggtcagtggccac   -1698

-1697   cagtcacctcctgggtgcatcccaggactcctggtctaaggccgtggccagaatcactcg   -1638

-1637   gtgcccaccccacccccagcacccctgtgccctttgctctgtgtctctgggtgaatccgg   -1578

-1577   ggccccagaagctccctcctcagggcacagaggccaaagatggggctgactgggggctgc   -1518

-1517   caccgggctttgggtgctgagggggctgtgggaccccaggggaagaggtgccgctccccc   -1458

-1457   cagcaccgggcactcccccgcctcccccggcctccagccctgcacaaagcagcttgccac   -1398

-1397   acccttcccaccaaggcccagggctgaggcctgcccaggacgcagggtgtggggaccctg   -1338

-1337   ctgagggagggtcccggaagaggggcttccctggcacagaggtccctctcagcaggcca   -1278

-1277   ggtgcggctgcctcagcacagtgtggggcggaggtgcaggacaaggttcccttccgcacc   -1218

-1217   taataccccagggtcaggccagcgccagcgctgctagtggcaacatggccccttcaaaga   -1158

-1157   ccccgtgtgcagagccagtcagcgtgcgctgtgttttctggggggccagccacttttttcc   -1098

-1097   ttaacagggtgacaaaccagacatcggggtgcggggacttcacgatatgcctctctaatg   -1038

-1037   gcgcgtgctacctcgcgtgtggtgggcagtgctgggcatgtggctgcgttccgggccctg   -978

-977    cagccgctcctccctctcctggggtctgaggtgtgggcaccctgtggcccgtttggggg   -918

-917    cctggagggagccccagtgcccaccgccctcggtgccctcagctgcagcctccccattcc   -858
```

```
-857  ctggggcctgccacgccctccactgcctcaaggatgcgtctgagcctggcctgcacatcc  -798

-797  atgctcccaccggctggaggggggtgttctggggccctggggggaccgtatatctggggagg  -738

-737  gggagggatccgccctaggggtgctgtgtggtgccccatagccaggcaagtctgaggtgg  -678

-677  acggcccgtcctcgccttgtgagcgaggcagagctgagctgagctgcccctcctgcctaa  -618

-617  cacgccactgtctctggagatcgggctgtgcgtgaacatgcggagcctgccctggtacgt  -558

-557  cccggccaaccccgactccttcttcccacgctgctacagcctctgcaccgagagtgagca  -498

-497  gcaggagttcctggggtaagtgaggagacggcagagggccccagtgctgtcagcagagagg  -438

-437  cttctagaaagatccccctggtgctgagacagactgatggggcagggtctgaggatagag  -378

-377  gaccgggggagaggcctcccatggtcatggtcatggcagtacagaggccagggggccccggg  -318

-317  agggagggcgggcagtcaaggagtgtgtggttctgtgctaggcttgtggacagcgcggcg  -258

-257  agcagctggggcaaggccggctccgtggtcggaggccgaggggtgcagctggacggccgc  -198

-197  agtcacagagacactgcagggagaagggcaggcagactgggggtgtgggagcaggcctgg  -138

-137  gccccatcggctatgagggcgggaagtggggcgggttggggagcctccgtggccctggcc  -78

-77   ccatctccagtccccagtcctggctcggacagatagggcgaggctgtgctgtcctttcag  -18

-17   aagacttccggcgcaccatggcatccagcatcctcaagtgggtggtcagccaccagagct  42
   1                 M   A   S   S   I   L   K   W   V   V   S   H   Q   S   C   15

  43  gcagcaggagcagcagaagcaagcccagggaccagagggaggaggccgggagcagcgacc  102
  16    S   R   S   S   R   S   K   P   R   D   Q   R   E   E   A   G   S   S   D   L   35

 103  tgagcagcaggcaaggtgcgctgggccgggggcagggcagtgccaggccaccagagctcgg  162
  36    S   S   R   Q   G   A   L   G   R   G   R   A   V   P   G   H   Q   S   S   G   55

 163  ggcctccacaggggccctccc  183
  56    P   P   Q   G   P   S   61
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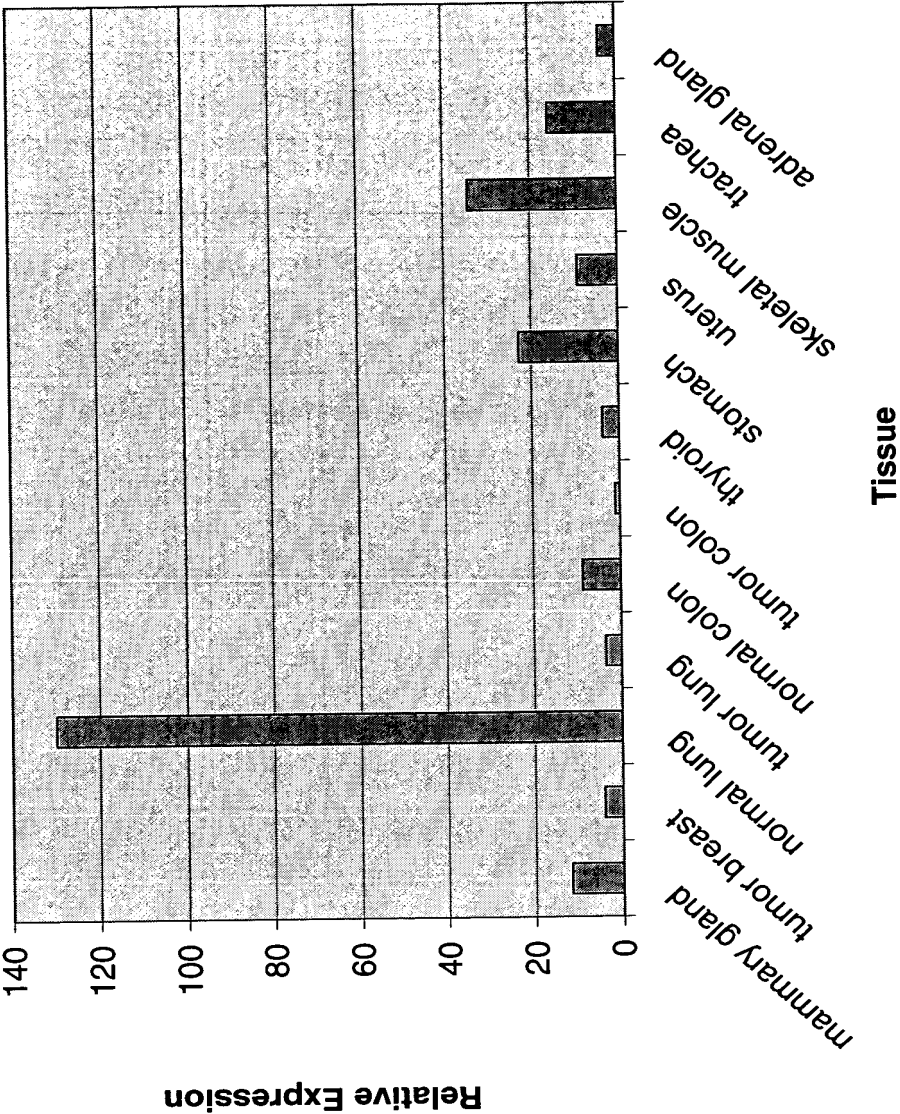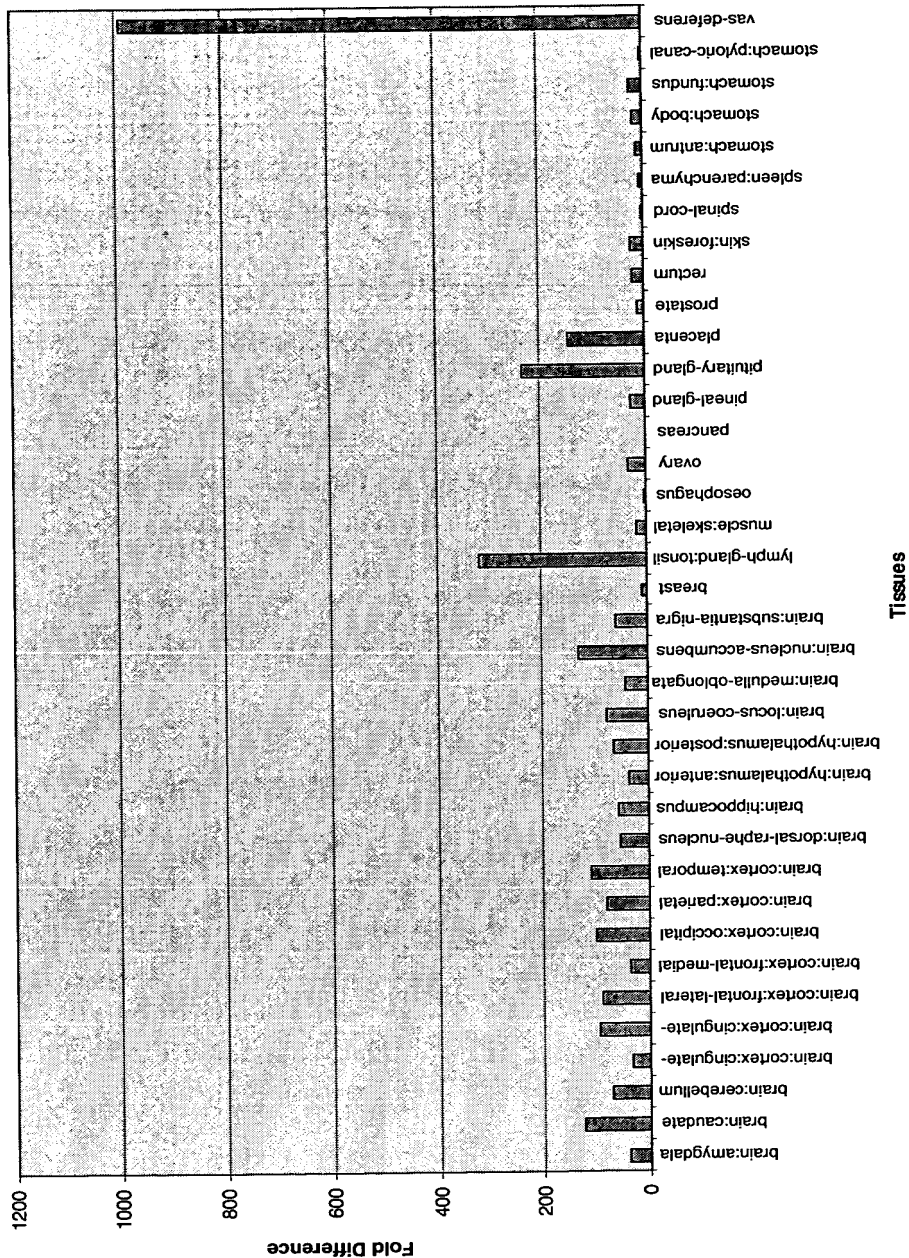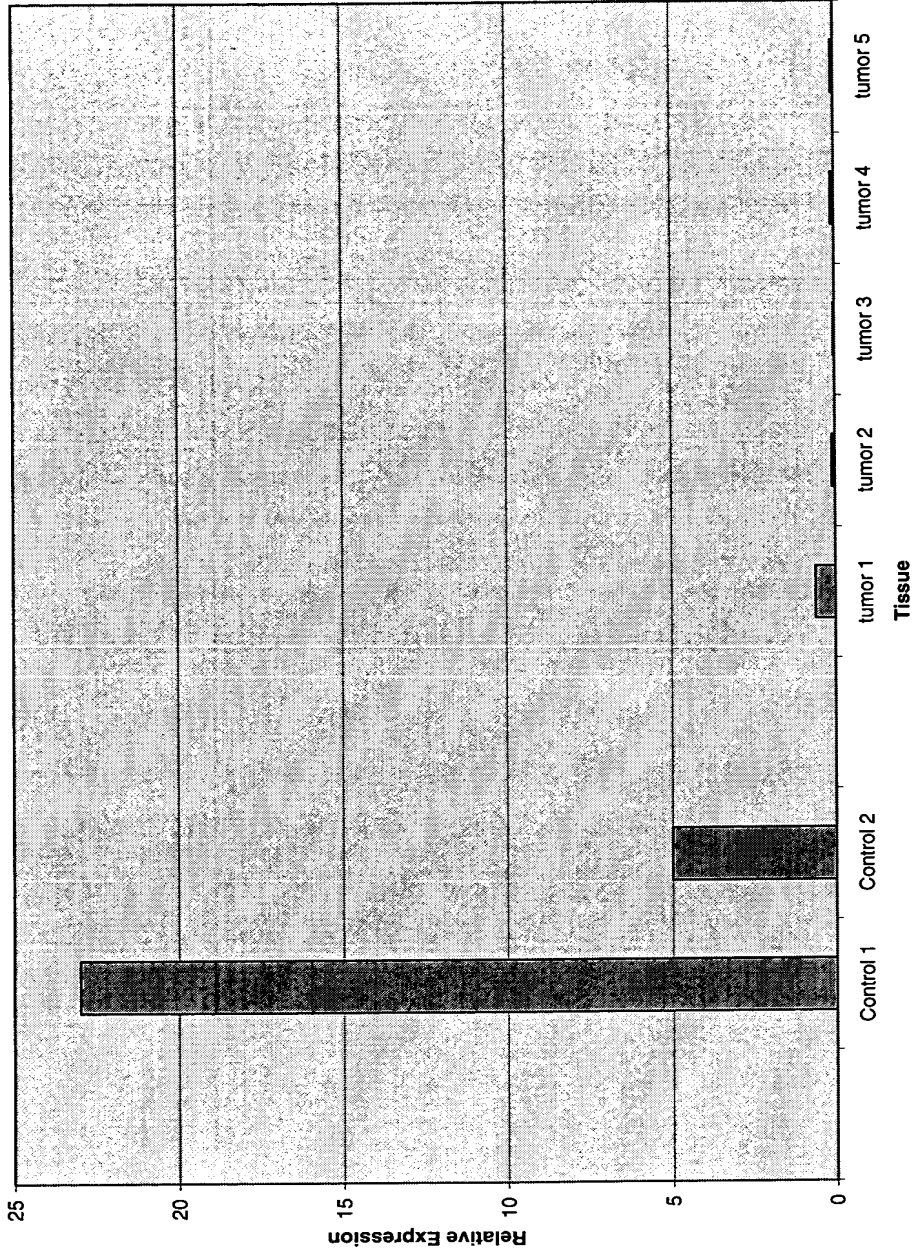
FIG. 8

FIG. 9

Relative Expression / Tissue
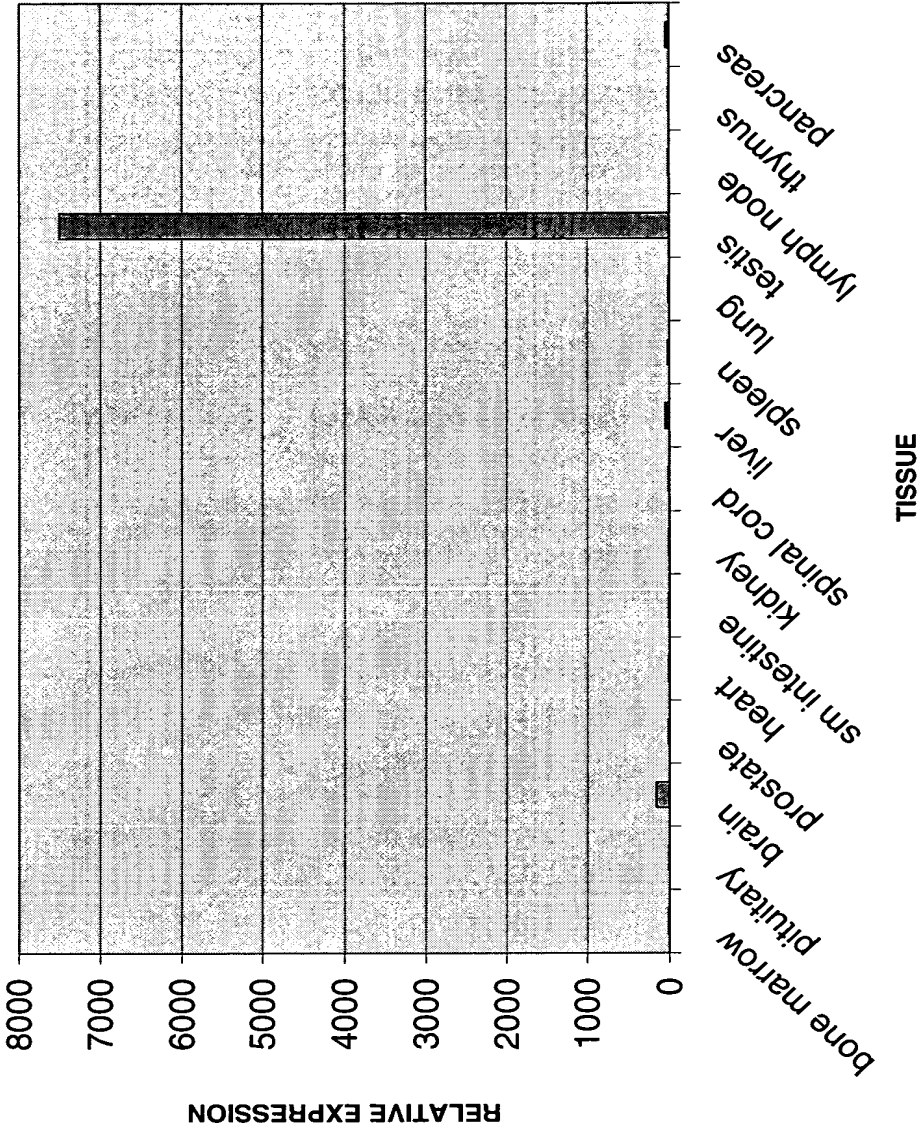
FIG. 10

FIG. 11

FIG. 12

Protein	Genbank ID	Identities	Similarities
Human HOTTL protein	gi|6683745	57.5%	65.5%
Pig tubulin--tyrosine ligase protein (TTL)	gi|423218	29.4%	40.0%
Human tubulin tyrosine ligase-like protein (TTLH_HUMAN)	gi|20455371	53.3%	61.4%
Human tubulin tyrosine ligase-like protein (TTLL_HUMAN)	gi|20455347	27.4%	38.4%